

SIMULATION OF THE FORMATION OF DNA DOUBLE STRAND BREAKS AND CHROMOSOME ABERRATIONS IN IRRADIATED CELLS

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The formation of DNA double-strand breaks (DSBs) and chromosome aberrations is an important consequence of ionizing radiation. To simulate DNA double-strand breaks and the formation of chromosome aberrations, we have recently merged the codes RITRACKS (Relativistic Ion Tracks) and NASARTI (NASA Radiation Track Image). The program RITRACKS is a stochastic code developed to simulate detailed event-by-event radiation track structure [1]. This code is used to calculate the dose in voxels of 20 nm, in a volume containing simulated chromosomes [2]. The number of tracks in the volume is calculated for each simulation by sampling a Poisson distribution, with the distribution parameter obtained from the irradiation dose, ion type and energy. The program NASARTI generates the chromosomes present in a cell nucleus by random walks of 20 nm, corresponding to the size of the dose voxels [3]. The generated chromosomes are located within domains which may intertwine [4]. Each segment of the random walks corresponds to ~2,000 DNA base pairs. NASARTI uses pre-calculated dose at each voxel to calculate the probability of DNA damage at each random walk segment. Using the location of double-strand breaks, possible rejoining between damaged segments is evaluated. This yields various types of chromosome aberrations, including deletions, inversions, exchanges, etc. By performing the calculations using various types of radiations, it will be possible to obtain relative biological effectiveness (RBE) values for several types of chromosome aberrations.

References:

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